

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:50:44 ; Search time 59.03 Seconds

(without alignments)
82.058 Million cell updates/sec

Title: US-09-785-059-1

Perfect score: 135

Sequence: 1 RVIRVORACRAIRHIVRIHQGRRL 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.19.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	83.0	854	15	056319 simian-huma
2	112	83.0	856	15	092877 simian-huma
3	112	83.0	856	15	074599 human immun
4	112	83.0	856	15	090SM7 human immun
5	111	82.2	852	15	089797 human immun
6	111	82.2	854	15	092762 human immun
7	110	81.5	856	15	077694 human immun
8	110	81.5	855	15	09JAC1 human immun
9	106	78.5	855	15	074841 human immun
10	106	78.5	855	15	092874 human immun
11	106	78.5	859	15	092937 human immun
12	106	78.5	866	15	073301 human immun
13	105	77.8	853	15	056108 human immun
14	104	77.0	860	15	09DH01 human immun
15	104	77.0	861	15	09E527 human immun
16	104	77.0	861	15	09E523 human immun

17	104	77.0	862	15	093024 human immun
18	104	77.0	872	15	091U21 human immun
19	104	77.0	872	15	091U20 human immun
20	103	76.3	357	15	078100 human immun
21	103	76.3	856	15	074090 human immun
22	103	76.3	860	15	09E534 human immun
23	103	76.3	860	15	09E518 human immun
24	103	76.3	862	15	09DVL5 human immun
25	102	75.6	853	15	056563 human immun
26	102	75.6	853	15	073372 human immun
27	102	75.6	858	15	071974 human immun
28	102	75.6	859	15	079924 human immun
29	101	74.8	136	15	079566 human immun
30	101	74.8	849	15	09PXE5 human immun
31	101	74.8	851	15	078243 human immun
32	101	74.8	858	15	091U25 human immun
33	101	74.8	869	15	090RE6 human immun
34	101	74.8	883	15	090RE5 human immun
35	100	74.1	856	15	0902G3 human immun
36	100	74.1	860	15	073309 human immun
37	100	74.1	861	15	091U24 human immun
38	100	74.1	863	15	041552 human immun
39	100	74.1	869	15	073302 human immun
40	99	73.3	56	15	056181 human immun
41	99	73.3	56	15	056182 human immun
42	99	73.3	56	15	056183 human immun
43	99	73.3	56	15	056184 human immun
44	99	73.3	56	15	056185 human immun
45	99	73.3	56	15	056199 human immun

ALIGNMENTS

RESULT 1
ID 056319 PRELIMINARY; PRT; 854 AA.
AC 056319;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHIV-89.6;
RX MEDLINE=96186751; PubMed=8627800;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
RA Sodroski J., Letvin N.L.;
RT "An env gene derived from a primary human immunodeficiency virus type
1 isolate confers high in vivo replicative capacity to a chimeric
simian/human immunodeficiency virus in rhesus monkeys.";
RT J. Virol. 70:3198-3206(1996).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=SHIV-89.6;
RA Reimann K.A., Li J.T., Voss G., Lekutis C., Tenner-Racz K., Racz P.,
RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Collman R.G.,
RA Sodroski J., Letvin N.L.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF038398; AAB9966.1; -;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97265 MW; 72AAB1531DICEAF7 CRC64;

Query Match 83.0%; Score 112; DB 15; Length 856;
Best Local Similarity 85.7%; Pred. No. 1.5e-07;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHVRIRROGLRRL 28
DB 828 RVIEVQACRAIRHVRIRROGLRRL 853

RESULT 2
092877 PRELIMINARY; PRT; 856 AA.

AC 092877;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_Taxid=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098984; Pubmed=9882298;
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
RT responsible for the pathogenicity of a multiply passaged simian-human
RT immunodeficiency virus (SHIV-HXB2).";
RL J. Virol. 73:976-984(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF041850; AAD12142.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00517; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 83.0%; Score 112; DB 15; Length 856;
Best Local Similarity 85.7%; Pred. No. 1.5e-07;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHVRIRROGLRRL 28
DB 828 RVIEVQACRAIRHVRIRROGLRRL 855

RESULT 3
074599 PRELIMINARY; PRT; 856 AA.

ID 074599;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MK1;
RX MEDLINE=90101366; Pubmed=1688473;
RA ClOyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
RT (HIV-1) Isolates.";

RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MK1;
RA Iwatsani Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86066; BAA12995.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 83.0%; Score 112; DB 15; Length 856;
Best Local Similarity 85.7%; Pred. No. 1.5e-07;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHVRIRROGLRRL 28
DB 828 RVIEVQACRAIRHVRIRROGLRRL 855

RESULT 4
090SM7 PRELIMINARY; PRT; 856 AA.

ID 090SM7;
AC 090SM7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HXB2;
RA Ataman-Onal Y., Cheynet V., Verrier B.;
RT "Mutations and transcriptional alterations associated with the
RT downregulation of HIV-1 envelope glycoprotein expression following
RT acute cytopathic effects.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF358141; AAK49977.1; -
SQ SEQUENCE 856 AA; 97126 MW; 9458D02B2FD734B3 CRC64;

Query Match 83.0%; Score 112; DB 15; Length 856;
Best Local Similarity 85.7%; Pred. No. 1.5e-07;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHVRIRROGLRRL 28
DB 828 RVIEVQACRAIRHVRIRROGLRRL 855

RESULT 5
089797 PRELIMINARY; PRT; 852 AA.

ID 089797;
AC 089797;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE ENVELOPE GLYCOPROTEIN.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=LM90-2;
RX MEDLINE=95127297; Pubmed=7826699;

RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HTLV type IIIB).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-LW90-2;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U12053; AAA76685.1; -;
 DR EMBL: U12036; AAA76671.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS: Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane
 SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4E33CF CRC64;

Query Match 82.2%; Score 111; DB 15; Length 852;
 Best Local Similarity 82.1%; Pred. No. 2,1e-07;
 Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
 DB 824 RVIEVORACRAIRHIVRIROGLRRL 851

RESULT 6
 ID 092762 PRELIMINARY; PRT; 854 AA.
 AC 092762;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SFMHS.3;
 RX MEDLINE=98178716; PubMed=9519894;
 RA McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,
 RA Sheppard W.H.;
 RT "Diversity of the human immunodeficiency virus type 1 envelope
 RT glycoprotein in San Francisco Men's Health Study participants.";
 RL AIDS Res. Hum. Retroviruses 14:329-337(1998).
 DR EMBL: AF025754; AAC40591.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 854 AA; 97287 MW; AFD8A82B62C5B27D CRC64;

Query Match 82.2%; Score 111; DB 15; Length 854;
 Best Local Similarity 82.1%; Pred. No. 2,1e-07;
 Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
 DB 826 RVIEVORACRAIRHIVRIROGLRRL 853

RESULT 7
 ID 077694 PRELIMINARY; PRT; 856 AA.
 AC 077694;

DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENV POLYPEPTIDE.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CAMBRIDGE;
 RA McIntosh A.A., Karpas A.;
 RT "Nucleotide sequence of a Cambridge isolate of human immunodeficiency
 RT virus type 1.";
 RL Submitted (MAR-1992) to the EMBL/Genbank/DBJ databases.
 DR EMBL: D10112; BAA00998.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 856 AA; 97493 MW; 19D32F205A94410D CRC64;

Query Match 81.5%; Score 110; DB 15; Length 856;
 Best Local Similarity 82.1%; Pred. No. 3e-07;
 Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
 DB 828 RVIEVORACRAIRHIVRIROGLRRL 855

RESULT 8
 ID 09JAC1 PRELIMINARY; PRT; 859 AA.
 AC 09JAC1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE PROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VH;
 RA Oelrichs R.;
 RT "Near full-length proviral sequence of HIV-1 from an individual
 RT homozygous for the delta-32 CCR5 allele.";
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF146728; AAF31326.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 859 AA; 97877 MW; 4C57D33D6FCDBF70 CRC64;

Query Match 81.5%; Score 110; DB 15; Length 859;
 Best Local Similarity 82.1%; Pred. No. 3e-07;
 Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RVIRVORACRAIRHIVRIROGLRRL 28
 DB 831 RVIEVORACRAIRHIVRIROGLRRL 858

RESULT 9
 ID 074841 PRELIMINARY; PRT; 855 AA.
 ID 074841

AC Q74841;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENV.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HAN-2;
 RX MEDLINE=90303973; PubMed=2364020;
 RA Sauermann U., Schneider J., Mous J., Brunnkhorst U., Schedel I.,
 RA Jentsch K.D., Hunsmann G.;
 RT "Molecular cloning and characterization of a German HIV-1 isolate."
 RL AIDS Res. Hum. Retroviruses 6:813-823(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HAN-2;
 RA Bryant B.W.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U03141; AA85237.1; -
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SO SEQUENCE 855 AA; 97507 MW; EF3CB615A23992F9 CRC64;

Query Match 78.5%; Score 106; DB 15; Length 855;
 Best Local Similarity 78.6%; Pred. No. 1.1e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVQACRAIRHIVRRIRGRLRL 28
 DB 827 RVIEVQACRAIRHIVRRIRGRLRL 854

RESULT 10
 ID 092874 PRELIMINARY; PRT; 858 AA.
 AC 092874;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHI146;
 RX MEDLINE=99372987; PubMed=10445815;
 RA Altman-Onal Y., Coiffier C., Giraud A., Babic-Ercceg A., Biron F.,
 RA Verrier B.;
 RT "Comparison of complete env gene sequences from individuals with
 RT symptomatic primary HIV type 1 infection."
 RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
 DR EMBL; AF041127; AAC02518.1; -
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SO SEQUENCE 858 AA; 97396 MW; 8E43A641C9D1535F CRC64;

Query Match 78.5%; Score 106; DB 15; Length 858;
 Best Local Similarity 78.6%; Pred. No. 1.1e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVQACRAIRHIVRRIRGRLRL 28
 DB 830 RVIEVQACRAIRHIVRRIRGRLRL 857

RESULT 11
 ID 092937 PRELIMINARY; PRT; 859 AA.
 AC 092937;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV-1JC;
 RX MEDLINE=98440562; PubMed=9765443;
 RA Mwaengo D.M., Novembre F.J.;
 RT "Molecular cloning and characterization of viruses isolated from
 RT chimpanzees with pathogenic human immunodeficiency virus type 1
 RT infections."
 RL J. Virol. 72:8976-8987(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIV-1JC;
 RA Mwaengo D.M., Novembre F.J.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF049494; AAC68848.1; -
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SO SEQUENCE 859 AA; 97811 MW; E43A24CC8424B62 CRC64;

Query Match 78.5%; Score 106; DB 15; Length 859;
 Best Local Similarity 78.6%; Pred. No. 1.1e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RVIRVQACRAIRHIVRRIRGRLRL 28
 DB 831 RVIEVQACRAIRHIVRRIRGRLRL 858

RESULT 12
 ID 073301 PRELIMINARY; PRT; 866 AA.
 AC 073301;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96263682; PubMed=8924250;
 RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J.,
 RA Daniels R.S.;
 RT "An efficient method for the rescue and analysis of functional HIV-1
 RT env genes: evidence for recombination in the vicinity of the tat/rev
 RT splice site."
 RL AIDS 10:39-46(1996).
 DR EMBL; U36875; AAC5535.1; -
 DR InterPro; IPR000328; Env_Gp41.

DR InterPro; IPR000777; GP120.
 RN Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 866 AA; 98348 MW; 6482AF2FED4BD4A0 CRC64;

Query Match 78.5%; Score 106; DB 15; Length 866;
 Best Local Similarity 78.6%; Pred. No. 1.1e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHIVRIRIGLRRL 28
 DB 838 RVLEIVQACRAIRHIVRIRIGLRRL 865

RESULT 13

ID 056108 PRELIMINARY; PRT; 853 AA.

AC 056108;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=SFMS3.1;
 RX MEDLINE=98178716; PubMed=9519894;
 RA McCutchan F.E.; Sanders-Buell E.; Salminen M.O.; Carr J.K.;
 RA Sheppard W.H.;
 RT "Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in San Francisco Men's Health Study participants."; AIDS Res. Hum. Retroviruses 14:329-337(1998).
 RL EMBL; AF025751; AAC40589.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 853 AA; 96830 MW; EC8BA4418F8AEC47 CRC64;

Query Match 77.8%; Score 105; DB 15; Length 853;
 Best Local Similarity 78.6%; Pred. No. 1.5e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHIVRIRIGLRRL 28
 DB 825 RVLEIVQACRAIRHIVRIRIGLRRL 852

RESULT 14
 ID 09DH01 PRELIMINARY; PRT; 860 AA.

AC 09DH01;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE ENV PROTEIN.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=20457217; PubMed=11000225;
 RA Yuste E.; Lopez-Galindez C.; Domingo E.;
 RT "Unusual Distribution of Mutations Associated with Serial Bottleneck Passages of Human Immunodeficiency Virus Type 1.";

RL J. Virol. 74:9546-9552(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yuste E.; Lopez-Galindez C.; Domingo E.;
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF256211; ANG16849.1; -
 DR EMBL; AF256205; ANG16800.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 860 AA; 97682 MW; 963E5DF9832F8A32 CRC64;

Query Match 77.0%; Score 104; DB 15; Length 860;
 Best Local Similarity 78.6%; Pred. No. 2.1e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHIVRIRIGLRRL 28
 DB 832 RVLEIVQACRAIRHIVRIRIGLRRL 859

RESULT 15

ID 09E527 PRELIMINARY; PRT; 861 AA.

AC 09E527;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENV PROTEIN.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=20457217; PubMed=11000225;
 RX Yuste E.; Lopez-Galindez C.; Domingo E.;
 RT "Unusual Distribution of Mutations Associated with Serial Bottleneck Passages of Human Immunodeficiency Virus Type 1.";
 RL J. Virol. 74:9546-9552(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yuste E.; Lopez-Galindez C.; Domingo E.;
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF256206; ANG16808.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR Pfam; PF00517; GP41; 1.
 KW Transmembrane.
 SQ SEQUENCE 861 AA; 97645 MW; DD0D135B595424E8 CRC64;

Query Match 77.0%; Score 104; DB 15; Length 861;
 Best Local Similarity 78.6%; Pred. No. 2.1e-06;
 Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RVIRVQACRAIRHIVRIRIGLRRL 28
 DB 833 RVLEIVQACRAIRHIVRIRIGLRRL 860

Search completed: August 14, 2002, 10:59:19
 Job time: 515 sec

